

Figure 1A

1	ACAAATGACCGGGAGCCATGACGTCATCGGGGGCGCAGGAAAGCAGGTGCTCTGCTGCTT	60
1	M T G S H D V I G G A G K Q V L C C F	19
61	TTGCAAGCAGAGAAATAAGAGTTTGGGCACCTACCCAGGGGTCCCAGGGAATGCCCTGTG	120
20	C K Q R N K S L <u>G T Y P G V P G N A L W</u>	39
121	GCTCCTGACCTCCCCCGCTGTAATGCTCTGAGCACTTCAGCAGTAATGCATGGAAGAGA	180
40	<u>L L T S P A C N A L S T S A</u> V M H G R D	59
181	TAAGGGGTCTGTGACCCATGGAAGTGTCCAAGTCCTCTCTGACACCCGCTTCTTTTCCTG	240
60	K G S V T H G T V Q V L S D T R F F S C	79
241	CCGTGAAGGACTACTTCCAGCAACCCAGTCTCCTGCCATGTCCGACCCCATCACGCTGAA	300
80	R E G L L P A T Q S P A M S <u>D P I T L N</u>	99
301	CGTCGGGGGAAGCTCTATACAACCTCACTGGCGACCCTGACCAGCTTCCCTGACTCCAT	360
100	<u>V G G K L Y T T S L A T L T S F P D S M</u>	119
361	GCTAGGCGCCATGTTTCAGCGGGAAGATGCCACCAAGAGGGACAGCCAGGGCAACTGCTT	420
120	<u>L G A M F S G K M P T K R D S Q G N C F</u>	139
421	CATTGACCGTGACGGCAAAGTGTTCGCTATATCCTCAACTTCCTGCGGACCTCCACCT	480
140	<u>I D R D G K V F R Y I L N F L R T S H L</u>	159
481	TGACCTGCCTGAGGACTTCCAGGAGATGGGGCTGCTCCGCAGGGAGGCCGACTTCTACCA	540
160	<u>D L P E D F Q E M G L L R R E A D F Y Q</u>	179
541	GGTGCAGCCCCTGATTGAGGCCCTGCAGGAGAAGGAAGTGGAGCTCTCCAAGGCCGAGAA	600
180	<u>V Q P L I E A L Q E K E V</u> E L S K A E K	199
601	GAATGCCATGCTCAACATCACACTGAACCAGCGTGTGCAGACGGTCCACTTCACTGTGCG	660
200	N A M L N I T L N Q R V Q T V H F T V R	219
661	CGAGGCACCCCAGATCTACAGCCTCTCCTCTTCCAGCATGGAGGTCTTCAACGCCAACAT	720
220	E A P Q I Y S L S S S S M E <u>V F N A N I</u>	239
721	CTTCAGCACCTCCTGCCTCTTCCTCAAGCTCCTTGGCTCTAAGCTCTTCTACTGCTCCAA	780
240	<u>F S T S C L F L K L L G S K L F Y C S</u> N	259
781	TGGCAATCTCTCCTCCATCACCAGCCACTTGCAGGACCCCAACCACCTGACTCTGGACTG	840
260	G N L S S I T S H L Q D P N H L T L D W	279
841	GGTGGCCAATGTGGAGGGCCTGCCAGAGGAGGAGTACACCAAGCAGAACCTCAAGAGGCT	900
280	V A N V E G L P E E E Y T K Q N L K R L	299

Figure 1B

901 CTGGGTGGTCCCCGCCAACAAAGCAGATCAACAGCTTCCAGGTCTTCGTGGAAGAGGTACT 960
300 W V V P A N K Q I N S F Q V F V E E V L 319

961 GAAATCGCTCTGAGCGATGGCTTCTGCATCGATTCTTCTACCCACATGCTCTGGATTT 1020
320 K I A L S D G F C I D S S H P H A L D F 339

1021 TATGAACAATAAGATTATTCGATTAATACGGTACAGGTAAAAGGACCCCAACAACACTGG 1080
340 M N N K I I R L I R Y R 351

1081 AGATGGGGAGTCCCAGGAAGCTCATGTCAGCCAGGTCTTGGAGGGCATCTCGCCAGTGGT 1140

1141 GCGAGGCAGGGGACTATACTAATCTGTATTAATTGTGTAGCAGGACTTGATTCCCCCAT 1200

1201 GATGAAGTCCACCTTTTGGAAATCCAGTGTCTCTGAACAGAACCACCTTTTTTCTTGCCA 1260

1261 TTTTGAGCTGCAGACAGGCGGTTTATTATGACAAGTGAAGAGTCAGCTGATGTGTACTAA 1320

1321 AGGAGGCCATAGGAGGATTTTCCAGCCAGGACAAAAGAGCAGCAGTTTTCTCCTGGGCTC 1380

1381 CATCTCTCTGTACCGCTAGCCAGTGCCGCATTTATCCATCTGTAAGAAGGCCCTGGTGA 1440

1441 GAGGATGGGATGAGAACAAGAGGCTACCTCCAGTTAACCAGGACATAAAGTCCCCAGCGG 1500

1501 TTCCTGTACACCTGCTCCTCCCTCCCCAGGGTGCATCCATGATCGTGGATGTTTGCCCA 1560

1561 GGGGTGACCATGTTTGGCTGGCTTGAATGCTGTGCATTCTCAGAGCTCTGTTAGTGTCC 1620

1621 CCTCTTGGGGGTCAGAGATGAGGTGTGGCAGGGTCTAGAGGAATGAGTGTCCAGGCAGAG 1680

1681 TTCAGAAGGTAGGAATGTCCCTCTTGATAGGGCTGAATCAAGGGATTCTTGCTTTAGAA 1740

1741 AGGGTCTGCTATCTTTGCAAAAATGTGCAAGTATCTGTAGCCAGTGTAATGAAATCACTT 1800

1801 CCAAATCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1839

Figure 2A

		1		50
K+betaM4	(1)	-----	MTGSHDVIGGAGKQVLCCFCKQRNKS LGTYPGVPGNALWLLT	
KCNMB1	(1)	-----		
K+Hnov28	(1)	-----		
K+Hnov27	(1)	-----		
CG10440	(1)	MDRERERDVKALEPRDLSSTGRIYARSDIKISSSPTVSPTISNSSSPTPT		
gi.12654691	(1)	-----		
		51		100
K+betaM4	(43)	SPACNALSTSAVMHGRDKGSVTHG----	TVOVLS DTRFFSCREGLPATO	
KCNMB1	(1)	-----	MVKKL VMAQKRCEPRALC	
K+Hnov28	(1)	-----	MDNGDW	
K+Hnov27	(1)	-----	MSRPLITRSPASPLXNOGIPPAQ	
CG10440	(51)	PEASSSVTPLGLPGAVAAAAA VCGASSAGASSYLHGNHKPITGIPCVAA		
gi.12654691	(1)	MPHRKERPSGSSLHTHGSTGTAE GGNMSRLSLITRSPVSPLAACGIPLPAAQ		
		101		150
K+betaM4	(89)	SEAMSDPITLNVGCKLYTISLATLTSEPD SMLGAMFSGKMP TKRDSQ-GN		
KCNMB1	(19)	LEVIMVCAVITFYILVTIVLPLYQKSVWTOESKCELIETNIRDOHELK		
K+Hnov28	(7)	GYMMDPVTLNVGGHLYTISLATLT RYPDSMLGAMFGGDFPTARD EQ-GN		
K+Hnov27	(25)	LTKSNAPVHIDVGGHMYTSSLATLT KYPESRIGRLFDGTEPIVLDSLKQH		
CG10440	(101)	ASRYDAPVHIDVGGITITSSLETLT KYPESKLAKLFNGQIPIVLDSLKQH		
gi.12654691	(51)	LTKSNAPVHIDVGSIMYTSSLATLT KYPDSRIISRLFNGTEPIVLDSLKQH		
		151		200
K+betaM4	(138)	CFIDRDGKVFYRILNFLRTSILDL PEDFOEMGLLRREADFYOMPILEAL		
KCNMB1	(69)	KKVPQYPCLVNVSAAGRWAVLYHTEDTRDQ NQQCSYIPGSVDNYQTARA		
K+Hnov28	(56)	YFIDRDGPIFRYILNFLRTSELITL PLDFKEFDLLRKEADFYODEPIIQCL		
K+Hnov27	(75)	YFIDRDGOMFRYILNFLRTSKLLIPD DFKDYTLIYEAKYFOLQPMLEL		
CG10440	(151)	YFIDRDGGMFRITLNFMRNSRLIT AEDFPDLELLLEEARYVEVPMIKQL		
gi.12654691	(101)	YFIDRDGETFRYILSFLRTSKLLL PDDFKDFSLLIYEARYYOLQPMREL		
		201		250
K+betaM4	(188)	QEKVVELSKAEKNAMLNITLNQRVQTVHFTVREAPQIYS---	LSSSSMBV	
KCNMB1	(119)	DVEKVRKFKQ-----	EQQVFCFS---APRGNETS	
K+Hnov28	(106)	NDPKPLYPMD-----	TFEVVELS---STRKLSKY	
K+Hnov27	(125)	ERWKODRETG-----	RFSRECEC---LWVRVAPDL	
CG10440	(201)	ESMRKQVRVNGNYLVAPPTPPARHIKTSPTSASPECNYEVVALHISPD		
gi.12654691	(151)	ERWQOEQEQR-----	RRSRACDC---LWVRVAPDL	
		251		300
K+betaM4	(235)	FNANIESTSCLEFLKLLGSKLFYCSNENLSITSHLODPNHITLDWMANVE		
KCNMB1	(146)	VLFORLYCPQALLFSLFWPTFLLTGGLIIIAMVKSNOYLSITMAAQ----		
K+Hnov28	(133)	SNPVAVIITQLTITTKVHSLLEGISNYFTKWNKAMMDTRCQVSFTFCPC		
K+Hnov27	(152)	GERITLSGDKSLDEEVFPETGDMCNSVN-AGWNH-DSTHVIREFPLNGYC		
CG10440	(251)	GERIMLSAFRALDELFPESAOATQSSRSGVSWNOGDWQOTIRFPLNGYC		
gi.12654691	(178)	GERIALSGEKALIEVFPETGDVMCNSVN-AGWNQ-DPTHMIRFPLNGYC		
		301		350
K+betaM4	(285)	GLPEEFYTKQNLKRLWVVPANKQIN-SFOVEVEEVLKIAISDGFCIDSSH		
KCNMB1	(192)	-----		
K+Hnov28	(183)	DYHQEVSILRVHLMEYITKQCF TIRNTRVHHMSEANENTVEHNWTFCRLA		
K+Hnov27	(200)	HLNSVQVLERLQQRGFETIVSCGGGVDSQFSEYVLRREIRRTPRVPSVI		
CG10440	(301)	KLNSVQVLRLLNAGETIEASVGG----	QQFSEYLLARRVPM-----	
gi.12654691	(226)	RLNSVQDVL-----		

Figure 2B

		351		368
K+betaM4	(334)	PHALD	FMN	NKIIRLIRYR
KCNMB1	(192)	-----		
K+Hnov28	(233)	RKTD		
K+Hnov27	(250)	RIKQ	EPL	
CG10440	(339)	-----		
gi.12654691	(235)	-----		

Figure 3

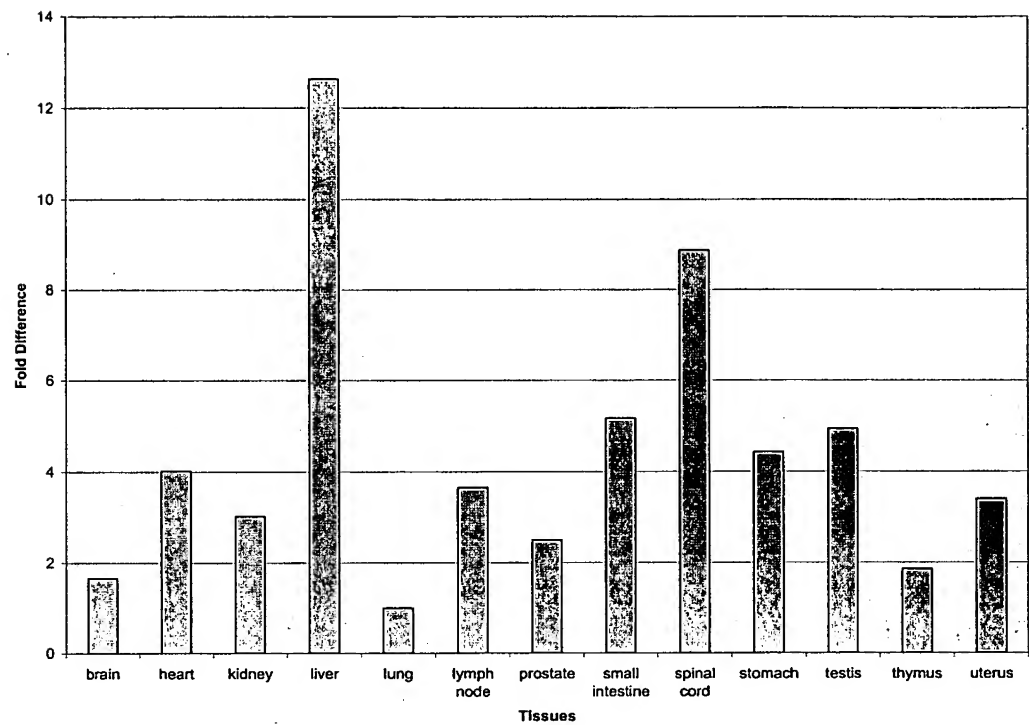


Figure 4.

K+betaM4

Protein	Genbank ID	Identities	Similarities
human potassium channel K+Hnov27 protein	gi Y34125	31.6%	45.1%
human potassium channel K+Hnov28 protein	gi Y34129	42.3%	50.5%
human neuroblastoma protein	gi 12654691	36.2%	47.3%
Drosophila CG10440 protein	gi 7291303	28.0%	38.6%
Human Maxi-K potassium channel beta subunit, KCNMB1	gi 4758625	26.1%	39.1%

K+betaM5

Protein	Genbank ID	Identities	Similarities
human potassium channel K+Hnov28 protein	gi Y34129	31.7%	43.4%
the human lung protein, MGC:2376	gi 12654469	34.4%	45.6%
human MSTP028 protein	gi 11640564	31.7%	43.4%
Caenorhabditis K+ channel tetramerisation domain containing protein	gi 3875362	34.4%	45.6%
Drosophila CG10465 protein	gi 7302243	30.8%	38.3%
Human Maxi-K potassium channel beta subunit, KCNMB1	gi 4758625	20.0%	40.0%

Figure 5

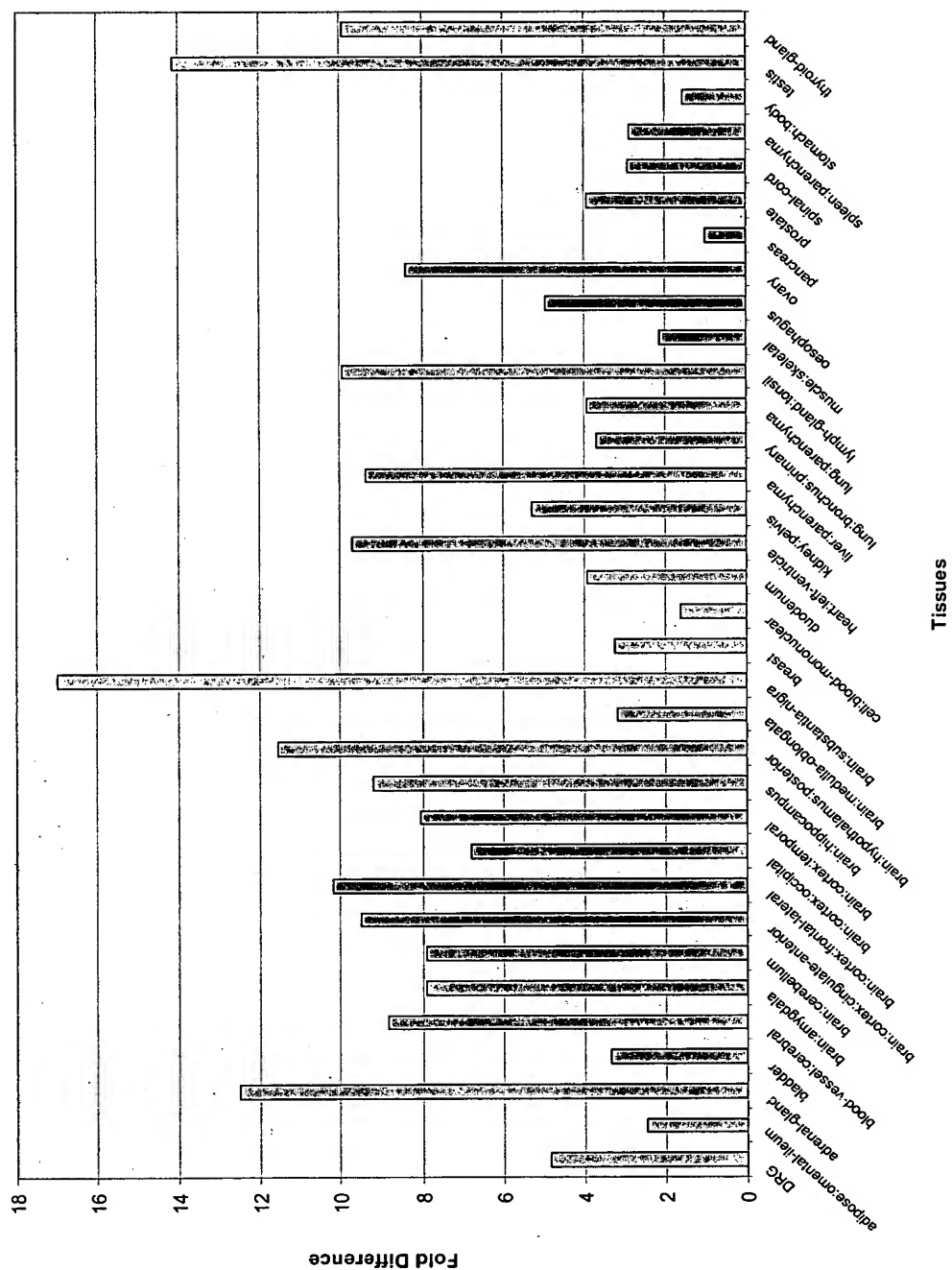


Figure 6A

1	ATGACGATGGCGGTTTTGCGGAATAGAAAAGGGGGAAAGGGGACCACTCAGGCGCCGGCCG	60
1	M T M A V L R N R K G G K G P L R R R P	20
61	CTGGCGCTGCCTGCTCTTCGACTGGGCGAGCTTCCTGCCAATCAGGGCGGAACCAGCGCG	120
21	L A L P A L R L G E L P A N Q G G T S A	40
121	GCGTCGGCCAGTAGCGGGAGGCGGTCTGGGTCAGGCCCCAGCTGGGCGCGAGCGGGTCGGC	180
41	A S A S S G R R S G Q A P A G R E R V G	60
181	GTTGAGGGAGCCACCGCCCTCCCGCCTGCGCACTGCCTCTCGCCCCCTCCGGCCAGCCC	240
61	V E G A T A L P P A H C L S P P S G Q P	80
241	GCAGCCGGCCGCGTCATGCCAGGCGCTGCTCGGCGAGCCAGAGGGATGGTGGTAGTCACG	300
81	A A G R V M P G A A R R A R G M V V V T	100
301	GGGCGGGAGCCAGACAGCCGTCGTCAGGACGGTGCCATGTCCAGCTCTGACCCGAAGAC	360
101	G R E P D S R R Q D G A M S S S D A E D	120
361	GACTTTCTGGAGCCGGCCACGCCGACGGCCACGCAGGCGGGGCACGCGCTGCCCTGCTG	420
121	D F L E P A T P T A T Q A G H A L P L L	140
421	CCACAGGAGTTTCCTGAGGTTGTTCCCTTAACATCGGAGGGGCTCACTTCACTACACGC	480
141	P Q E F P <u>E V V P L N I G G A H F T T R</u>	160
481	CTGTCCACACTGCGGTGCTACGAAGACACCATGTTGGCAGCCATGTTCACTGGGCGGCAC	540
161	<u>L S T L R C Y E D T M L A A M F S G R H</u>	180
541	TACATCCCCACAGACTCCGAGGGCCGGTACTTCATCGACCGAGATGGCACACACTTTGGA	600
181	<u>Y I P T D S E G R Y F I D R D G T H F G</u>	200
601	GATGTGCTGAATTTCTGCGCTCAGGGGACCTCCACCCAGGGAGCGTGTTTCGAGCTGTG	660
201	<u>D V L N F L R S G D L P P R E R V R A V</u>	220
661	TACAAAGAGGCCCAGTACTATGCCATCGGGCCCCTCCTGGAGCAGCTGGAGAACATGCAG	720
221	<u>Y K E A Q Y Y A I G P L L E Q L E N M Q</u>	240
721	CCACTGAAGGGCGAGAAGGTGCGCCAAGCGTTTCTGGGACTCATGCCCTATTACAAAGAC	780
241	<u>P L K G E K V R Q A F L G L M P Y Y K D</u>	260
781	CACTTGAGCGGATTGTGGAGATCGCCCGGCTGCGTGCGGTCCAGCGGAAGGCCCGCTTT	840
261	<u>H L E R I V E I A R L R A V Q R K A R F</u>	280

Figure 6B

841	GCCAAGCTCAAGAGCTTGACACCTTCCTGGCTAATGAGTGTCTCATCAAGATGCCCCCT	900
281	<u>A K L K S L T P S W L M S V L I K M P P</u>	300
901	GGAGTCACATCATGGATTAACGCAGAAAGGCGGCTGTATTTGGAAACTCCCATTGGTCCA	960
301	<u>G V T S W</u> I N A E R R L Y L E T P I G P	320
961	GAGAGACAGAACAAATGAGAAGAAATCCCCTGTCCAGTTGCCTGCAGGAGTATTCCAACAC	1020
321	E R Q N N E K K S P V Q L P A G V F Q H	340
1021	TTCATGGGCTAGAGGATTCCATTGAGATGGGGTTTACGTCTTGATTTTGAACACCTGTCA	1080
341	F M G	343
1081	GCACTGTTCTCTGTTTGCATGGCAATTCTGACCCTTTTATGGCAACAACACCCCTGGGAC	1140
1141	AACCCAGATTTGTAGATTGAGATCCAAAGGTAGAATTTCCAGACAGTCCAACCAAGGTAT	1200
1201	CAAGTGATGTTTCCAGAGTGGAAGGCTCTCACCGTGTCCAGGATTTCTGGGGTTTGTAA	1260
1261	GCAGTACTGGCCATTTGTGACCCTGTTTTTACCTAATCATTCTGTCTTTTTAGGACATG	1320
1321	GTTTTACCCGATCCCTGGCAAAGGATCCAGAATTCGAATAGCTGAAAACCCTGTTATAGC	1380
1381	TTTTCTCCTATTCTGCCTTACCCAAGACACACTTGAACCCCTCAGTAAGGCTATAGAGAG	1440
1441	GGCCATGAGCAGGGGCAGCCTCTCCCTTGTTTCTACAGCTCCATGATGAGGGGTTGACTG	1500
1501	AGGCCAGCAATCCTTGTTAGGTGTGACAGTTGCAATATAATTAACAGTTTCAAGATCTAGA	1560
1561	GGTACCTTTTGAAGAACCCTTCAGGGATATCTATCCACAGTAGCCTGGAGCAGCCAAG	1620
1621	GTGAACCTGAGATTTTGACCCACACAATAAGGGGGGGCCATTCTTTTTCAAATATTTTGG	1680
1681	CTTCAGAATACTTCATTACACATGCAAATATTGAGAGATTAACAGAAATTCCAGCTCT	1740
1741	TATGCCTAACTGAGAAGAGCCACTGCAAGTTGCAGTTAGGTACCCATGTGCAGCAGAGGC	1800
1801	CAGCTGAATCCCAGAGCTTCCCAAAGTGACACCAGCGGGGACTATTCTTGATGTCCAC	1860
1861	CCAAGAGAGGAAGATGAGCTGAGGCGCTCTTGCTCTGCCCAAATGCATCCCATGTGCATT	1920

Figure 6C

1921 CACGTGTCACCCATTCAAAATAACATGGCATTCTTGGAACCTTGTATCTGACATGTAAGA 1980
1981 CCAGCCTACACATTGGGGTGGGTGCAGGGGCTCACACTTGTAATCCTAGCACTTTGGAAG 2040
2041 GCTGAGGTGGGCAGATTGCTTGAGCACAGGAGTTCCAGACCAGCCTGAGCAACATGGCGA 2100
2101 AATCCTGTCTCTTCAAGAAATAAAATAATAATAATAAAAAAAAAAAAAAAAAA 2154

Figure 7A

		1	50
K+betaM5	(1)	MTMAVLNRNRKGGKGPLRRRPLALPALRLGELPANQGGTSAASASSGRRSG	
KCNMB1	(1)	-----	
CG10465	(1)	-----	
gi.12654469	(1)	-----	
K+Hnov28	(1)	-----	
MSTP028	(1)	-----	
K+channel_tetra	(1)	-----	
		51	100
K+betaM5	(51)	QAPAGRERVGVEGATALPPAHCLSPPSGQPAAGRVMPGAARRARGMVVVV	
KCNMB1	(1)	-----	
CG10465	(1)	-----	
gi.12654469	(1)	-----	
K+Hnov28	(1)	-----	
MSTP028	(1)	-----	
K+channel_tetra	(1)	-----	
		101	150
K+betaM5	(101)	GREPDSRRQDGAMSSSDAEDDFLEPATPTATQAGHALPLLQEFEEVPL	
KCNMB1	(1)	-----MVKKLVMA	
CG10465	(1)	-----MSEMSG-----DHKILLKGHS--SQYLLKL	
gi.12654469	(1)	-----MSTVEL	
K+Hnov28	(1)	-----MDNGDWGYMMDDPVTL	
MSTP028	(1)	-----MEEMSGESVSSAVPAAATRTTSFKGTSPSSKYVKL	
K+channel_tetra	(1)	-----MEPSTTVKL	
		151	200
K+betaM5	(151)	NVGGCHLYTTIRLSTLLRCYEDTMLAAMFSGRHYTPDSEGRYFIDRDGTHFG	
KCNMB1	(9)	QKRGETRALCLGVTMVCAVITYYLLVTTVLPYQKSVWTQESKCHLIET	
CG10465	(24)	NVGGCHLYTTIGTLTKNDMLSAMFSGRMEVLTDSGWIIDRCGNHFG	
gi.12654469	(8)	NVGGCHLYTTITLGLRKFPCKLAEMFSSLAKESTDAEGRFFIDRPSITYER	
K+Hnov28	(17)	NVGGCHLYTTISLTLTRYPDMLGAMFGCDPTARDPQGNFYIDRDGPFLFR	
MSTP028	(37)	NVGCALYTTTMTLLTK-QDMLKAMFSGRMEVLTDSGWIIDRCCKHFG	
K+channel_tetra	(10)	DVGCKKTKTTITFTLCK-HDSMLKTMFCTDVPVTKNEEGSVFIDRDGKHFR	
		201	250
K+betaM5	(201)	DVLNLSLRSCDLPP--REK-VRAVYKEAQYVAICPLLEQLENMQPLKGEK-	
KCNMB1	(59)	NIRDOELKGGKVPOYPCLWNVSAACRNNAVYHTESTRQONQCSYIPG	
CG10465	(74)	IILNMLRDGTIVPLPETNKEAEALLAEAKYYCTELALISCERALYAHQEPK	
gi.12654469	(58)	PILDMLRTGQVPT---QHTEVYREAOYVEIKPLVKKLLEDMPQIFGEQV	
K+Hnov28	(67)	YVLNLSLRTSELTLPLDFKEDLLRKEADEVOIEPLIQCLNDPKPLYPMD-	
MSTP028	(86)	TILNMLRDGAVPLPESRRETEELLAEAKYYLVQGLVEECQAAALQNKDTYE	
K+channel_tetra	(59)	LILNLSLRDQIALPDSDRREVRLAEASVSLMDPLLELCGERLEQSLNP-	
		251	300
K+betaM5	(247)	-----VROAFLG---LMPYYKHHLERLVEIAR-----LRVQR	
KCNMB1	(109)	SVDNMQARADVEKVRKAFQEQQVFYCESAPR-----	
CG10465	(124)	PICRPLPITSQKEEQLLSVSLKPAVILVVQRQNNKYSYTSSTDNMLKN	
gi.12654469	(104)	SRKQPLQVPGYSENLELMVRLARAEATTARK-----SSVVC	
K+Hnov28	(116)	---TEEVVELSSTRKLSKYSNPVAVITITQL-----TITTKVHSL	
MSTP028	(136)	PFCKVPVITSSKEEQKLITATSNKPAVKLLYNRSNNKYSYTSNSDDNMLKN	
K+channel_tetra	(108)	---YVHLVSTVLEARKLITAFIEKPIVVLRP-----VYIATSGNQSYYS	
		301	350
K+betaM5	(277)	KARFAKLKSLTPSWLMSVLIKMP-----GV--TSVINAERRLYLETPIGP	
KCNMB1	(141)	GNETSVLFQRLYGPQALLFSLFWP-----TELLTGGLLIHAMVKSNOY	
CG10465	(174)	TELFDKLSLRGNERITFLKQVIGP---SEICQWSEYGHGKQVAEVCCTSI	
gi.12654469	(142)	LVETEEQDAYMSEVLCFLQDKMFKSVVKFGPWKAVLDNSDLMHCMLEMDI	
K+Hnov28	(153)	LEGTSNYFTKWNKHMMDIRDCQVS---FTFGPCDYHQEVSLRVHMEYIT	
MSTP028	(186)	TELFDKLSLRNGRVLFLKQVIG---DEICQWSEYQGGRKTAEVCCTSI	
K+channel_tetra	(150)	ETKFRLESEEMHKHVAFLITEPEF--NEDCSWSEFLRAKKTARIKG-P	

Figure 7B

		351		400
K+betaM5	(321)	ERQNNK	KSPVQLPAGVFQHF	MG-----
KCNMB1	(184)	SILAA	QK-----	
CG10465	(221)	VYATDR	KHKVEFPEAR	IYEETLQVLLYENRN--APDQELMQATSSARVG
gi.12654469	(192)	KAQGYKVFS	KFYLTYP	TKRNEFHFNISFTFTW----
K+Hnov28	(200)	KQGFTIR	NTRVHHMSE	RANENTVEHNWTFCLARKTDD-----
MSTP028	(232)	VYATEK	KQKVEFPEAR	IYEETLNILLYEAQDGRGPDNALLEATG----
K+channel_tetra	(197)	MDCNLVE	ECMPKTVERR	REKKIWH-----
		401		440
K+betaM5	(344)	-----		
KCNMB1	(192)	-----		
CG10465	(269)	SASGTSINQYTSDEEEEERTGLARLSNKRNP	S-----	
gi.12654469	(226)	-----		
K+Hnov28	(238)	-----		
MSTP028	(277)	---	GAAGRSHHLDEDEERERI	ERVRRIRHIKRPDDRAHLHQ
K+channel_tetra	(221)	-----		

Figure 8

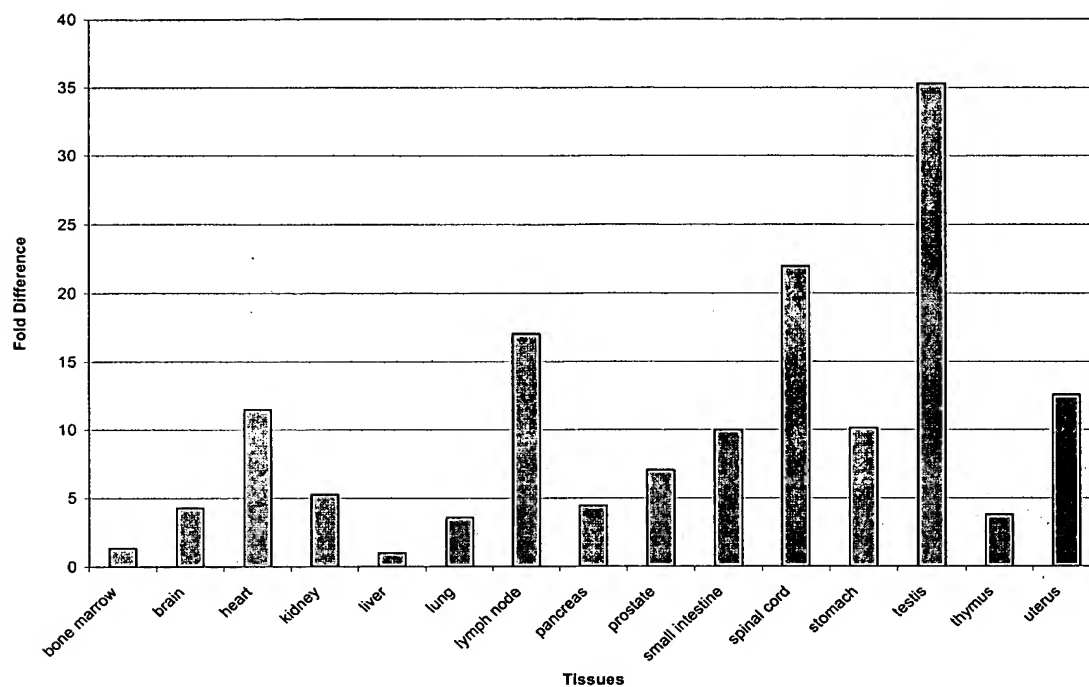


Figure 9

